Amendments to the Specification:

Please replace the paragraph beginning at page 1, line 4 with the following amended paragraph:

Cross-Reference to Related Applications

This application is a continuation of U.S. Application Serial No. 09/321,346, filed May 27, 1999, now abandoned, which is: a continuation-in-part of U.S. Application Serial No. 09/266,463, filed March 11, 1999, now abandoned; a continuation-in-part of U.S. Serial Number 09/003,253, filed January 6, 1998, now abandoned, which claims benefit of U.S. Provisional Application Serial Number 60/035,983, filed January 22, 1997; and a continuation-in-part of International Application PCT US/98/01499, filed January 22, 1998. The disclosures of the prior applications are considered part of and are incorporated by reference in the disclosure of this application.

Replace the paragraph beginning at page 4, line 31 with the following amended paragraph:

The determination of percent homology between two sequences can be accomplished using the algorithm of Karlin and Altschul (1990) *Proc. Natl. Acad. Sci. USA* 87:2264-2268, modified as in Karlin and Altschul (1993) *Proc. Natl. Acad Sci. USA* 90:5873-5877. Such an algorithm is incorporated into the NBLAST and XBLAST programs of Altschul et al. (1990) *J. Mol. Biol.* 215:403-410. BLAST nucleotide searches can be performed with the NBLAST program, score = 100, wordlength = 12, to obtain nucleotide sequences homologous to a nucleic acid molecule of the invention. BLAST protein searches can be performed with the XBLAST program, score = 50, wordlength = 3, to obtain amino acid sequences homologous to a protein molecule of the invention. To obtain gapped alignments for comparison purposes, Gapped BLAST can be utilized as described in Altschul et al. (1997) *Nucleic Acids Res.* 25:3389-3402. Alternatively, PSI-Blast can be used to perform an iterated search which detects distant relationships between molecules. *Id.* When utilizing BLAST, Gapped BLAST, and PSI-Blast

programs, the default parameters of the respective programs (e.g., XBLAST and NBLAST)

should be used. *See* http://www.ncbi.nlm.nih.gov.